Sig. Frame

0.00

1529 1020 1163

to: 1529

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SCORE (STDEV

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AHTEDAQGTTALRRYPADQNSSGPDAYEEVTDGAQTGGLGFNLRIGRPKGPRDPPAEW
                                                                                                                                                                                                                                                                                             house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cheng.J., Fennie,C. and Lasky,L.A.
Direct Submission
Submitted (23-FEB-1996) Laurence A. Lasky, Molecular Oncology,
Genentech Inc., 460 Pt. San Bruno Blvd., San Francisco, CA 94080,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAATICGGCACGAGCGGGCTGGACCTTGCTC-GCCGGGGGG--CATGAGCCGCAGCCTGGACTCGGCGCG
                                                                                                                                                                                                          MMPTPHSC 1529 bp mRNA ROD 08-NOV-1996
Mus musculus protein tyrosine phosphatase mRNA, complete cds.
U49953. GI:1293621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On May 2, 1996 this sequence version replaced g1:1277080 Location/Qualifiers
                  Init. Opt.
Length Score Score
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                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 1559)
Cheng, J., Daimaru, L., Fennie, C. and Lasky, L. A.
A novel protein tyrosine phosphatase expressed in
11n(10)CD34hiSca(hi) hematopoletic progenitor cells
Blood 88 (4), 1156-1167 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. 1529
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19. .1380
                                                                                                                 1. US-08-877-150B-35 (1-2810)
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                                 Sequence Name
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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                                                                                                                      Results file us-08-877-150b-35.res made by sdavid on Wed 24 Oct 101 13:40:59-PDT.
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                                                                                                                                                                            Query sequence being compared:US-08-877-150B-35 (1-2810)
Number of sequences searched:
Number of scores above cutoff:
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Joining penalty
Window size
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                                                                      FastDB - Fast Pairwise Comparison of Sequences
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Number of sequences searched:
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Mismatch renalty
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0.00 328 0

Significance -Mismatches -

The list of best scores is:

Scores:

Times:

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| 100 | 800 | 810 | 820 | 830 | 840 | 850 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 | 860 
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                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1529)
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San Bruno Blvd., San Francisco, CA 94080,
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Mus musculus protein tyrosine phosphatase mRNA, complete cds.
U49853
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Location/Qualifiers
1. .1529
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Length Score Score
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Mismatches
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A novel protein tyrosine phosphatase expressed in
lin(lo)CD34hiSca(hi) hematopoletic progenitor cells
Blood 88 (4), 1156-1167 (1996)
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Cheng, J., Fennie, C. and Lasky, L.A.
Defect Submission
Submitted (23.PFB-1996) Laurence A
Genentech Inc., 460 Pt. San Bruno
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u49853 TOIG of: u49853
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Residue Identity
                          Sequence Name
                                                     1. u49853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                    LOCUS
                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                    TOIG of:
                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      049853
                                                                                                                   24 Oct 101 13:42:24-PDT.
                                                                                                                                                                                                                           Results of the initial comparison of US-08-877-150B-35' (1-2810) with: File: u49853.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33,30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Standard Deviation 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A 100% identical sequence to the query sequence was not found
                                                                                                            Results file us-08-877-150b-35-inv.res made by sdavid on Wed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total Elapsed 00:00:00.00
                                                                                                                                                                  (1-2810)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K-tuple
Joining penalty
Window size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                         Query sequence being compared:US-08-877-150B-35'
Number of sequences searched:
Number of scores above cutoff:
                                                               FastDB - Fast Pairwise Comparison of Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEARCH STATISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Median
0
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00:00:00:00
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1.00
0.33
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98
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scores above cutoff:
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> 0 < Ol | O IntelliGenetics > 0 <
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Mismatch penalty
Cap penalty
Gap size penalty
Cutoff score
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                                                                                Release 5.4
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Number of
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                                                                                                                                                                                                                                                                                                                          50-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCORE
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0.00

4

The list of best scores is:

us-08-877-150b-35-inv.res

480	AGCTGGAGATGTGTACTCATTTGGGGGACTTGTCTGTCAATCTGGAGGATCATGTCTGACTAGCTGGGG 	
470	GATCATGTCT 	
460	CAATCTGGAG       -GGCCTGG	
450	CTTGTCTGT( 	
440	VTTTGGGGGA         CATTAAGGC 120	
430	TGTGTACTCA 	
420	AGCTGGAGA          CCTCGCTCGTGA	

| 840 | 870 | 880 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890 | 890

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 | 1570 | 1580 | 1590 | 1610 | 1620 | 1630 | 1630 | 1620 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 | 1630 |

 Sig. Frame

2.05

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/translation-"MSRHTDLVRSFLEQLEARDYREGAILAREFSDIKARSVAWKSEG
VCSTKAGSRLGNTNKNRYKDVVAYDETRVILSLLQEEGHGDYINANFIRGIDGSQAYI
ATGGPLPHTLLDFWRLVWEFGVKVILMACQETENGRRKCERYWAREQEPLKAGPFCIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLGFGPLCVHCSAGCGRTGVLCAVDYVRQLLLTQTIPPNFSLFQVVLEMRKQRPAAVO
TEBQYRELTHTVAQLESRTLQDTSPHYONLKBRCAPICKERSESLRTSSALPATSRPPG
GVLRSISVPAPPTLPADTTLQDYSRGASAGTGPGPRAPTSTDTPIYSQVAPRAQRPV
AHTEDAQGTTALRRVPADQNSSGPDATEBVTDGAQTGGLGFRIKBIGRRKGPRDPPAEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTKETTLNADITLRTLQVTFQKEFRSVHQLQYMSWPDHGVPSSSDHILTMVEEARCLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96329547
2 (bases 1 to 1529)
2 Cheng,J., Fennie,C. and Lasky,L.A.
Direct Submission
Submitted (23-FEB-1996) Laurence A. Lasky, Molecular Oncology,
Genentech Inc., 460 Pt. San Bruno Blvd., San Francisco, CA 94080,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1529)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMPTPHSC 1529 bp mRNA ROD 08-NOV-1996
Mus musculus protein tyrosine phosphatase mRNA, complete cds.
U49853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On May 2, 1996 this sequence version replaced gi:1277080,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Type: N Check: 2626
         Init. Opt.
Length Score Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheng, J., Dalmaru, L., Fennie, C. and Lasky, L.A. A novel protein tyrosine phosphatase expressed in lin(lo)2034hiSca(hi) hematopoletic progenitor cells Blood 88 (4), 1156-1167 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/cell_line="hematopoietic progenitor cell"
19. .1380
                                                         **** 2 standard deviations above mean ****
TOIG of: u49853 check: 2626 509 364
**** 0 standard deviation from mean ****
                                                                                                                                                                                                                                                   1. US-08-877-150B-36 (1-458)
u49853p_1 TOIG of: u49853 check: 2626 from: 1 to: 1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Optimized Score = 404
Matches = 347
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="tyrosine phosphatase"
/protein_id="AAB18623.1"
/db_xref="G1:1293622"
                                                                                                                                                                                                                                                                                                            from: 1 to: 1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 1529 October 24, 2001 13:28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                            TOIG of: u49853 check: 2626
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                           Description
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75%
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house mouse.
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Residue Identity
Gaps
                                                                                                                                     u49853p_6
u49853p_3
u49853p_2
u49853p_5
                                                                              1. u49853p_1
                                                                                                                    u49853p_4
                           Sequence Name
                                                                                                                                                                                                                                                                                                                                                LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                        Results file us-08-877-150b-36.res made by sdavid on Wed 24 Oct 101 13:51:52-PDT.
                                                                                                                                                                                                                                              Results of the initial comparison of US-08-877-150B-36 (1-458) with: File : u49853.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A 100% identical sequence to the query sequence was not found
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283
                                                                                                                                                                   Query sequence being compared:US-08-877-150B-36 (1-458)
Number of sequences searched:
Number of scores above cutoff:
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143.65
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Significance is calculated based on initial score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243
                                                   FastDB - Fast Pairwise Comparison of Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEARCH STATISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Median
12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202
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6
6
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00:00:00
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Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mean
70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sim.
IntelliGenetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity matrix
Threshold level of s
Mismatch penalty
Gap penalty
Gap size penalty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 off score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -0
                                                                        Release 5.4
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SCORE 0 STDEV

Scores:

Times:

2.05

Significance Mismatches

The list of best scores is:

X 10 MSRSLDSARSFL----ERLEA

-0.40 316 21

Significance Mismatches

Optimized Score = 205
Matches = 80
Conservative Substitutions

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APENPSWWPGCGROCKGORG -- EGFLADWSAV---LLEVLVVGAGVLESAGEXLSHCVVGEPVLLCLHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HNTLHSSMVVPGVQPPPSGRLXLAQHSLHPCPLCWRIPGPFGPSDAQVBAXPSSLCSICYFFVGIRPGRVLV
30 40 50 90
                                                                                                                                                                                                                                                                                                   20 30 70 80 RGGREGAVLAGEFSDIQACS ---AAWKADGVCSTV-AGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 100 110 120 150 XINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \frac{160}{\text{CITLIK}} - \text{EKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPDHMLAMVERARRQGSGPEPLCV}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 380 400 410 420 430 X GAGSGTQTGTG-TGARSAEEAPLXSKVTPRAQRPGAHAEDARGTLPGRVPADQSPAGSGAYEDVAGGAOTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRPLFPHLQDHLEETEVGRD-CLGQQQLPHIVNSAQDTCSSAASTAVDTEGSRSKPLEAAGLLHHGENVIRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HCSAGCGRIGVLCTVDYVRQLLLTQMIPPDFSL-FDVVLKMR--KQRPAAVQTEEQYRFLYHTVAQMFCSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | | | | | |
LTGHODYLDPKLPNQAPEVQCVRQGSLRRNVGLASIYAPDEVGIDVISMSLLLEQGKDDSCLIICYHIFVA
380 390 400 410 420 430 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNASPHYQNIK-ENCAPLYDDAL---FLRTPQALLAIPRPGGYLRSISVPGSPGHAMADTYAEEQKRGAPA
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            . . .
Initial Score
Residue Identity
Gaps
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Residue Identity
                                     320 330 380 PLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKRGAPAGAGSGTQTGTGARSAEE
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APLYSKVTPRAGRPGAHAEDA---RGTLPGRVPADQSPAGSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -0.36
78
7
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Mismatches
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SAGTRRSAVVPCASSVCATGRWARCATWLXIGVSVLVGARGPGPVPAEAPRFCTTA
100 110 120 130 140 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Optimized Score = 44
Matches = 12
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            390
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12%
3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 290
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```

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PGLPGGGNPRSXVQRHXGPLS-GLEVXRCVFHXSRQSAWEHEQEPLQRCGSIXXDKSIIPFPAPRGGTWRLHQ
                                                                                                                                                   350 360 370 380 390 400 410
GHAMADTYAEEQKRGAPAGAGSGTQTGTGTGARSAEEAPLYSKYTPRAQRPGAHAEDARGTLPGRVPADQSP
                                                                                                                                                                                                  SSGSQHESPYGLGEELLGAAGG
X
                                                                              -0.41
52
6
                                                                              Significance
Mismatches
                                                                          Optimized Score = 28
Matches = 3
Conservative Substitutions
                                                                                                                                                                                                                                                                 420 430 440 450 x AGGAYEDVAGAQTGGLGFNLRIGRPKGPRDPPAEWTRV
US-08-877-150B-36 (1-458)
u49853p_3
                                                                              11
4 %
                                                                                                                                                                                                                                                                                                                                                                                  CQLHPGHRWKPGLHCDAR
```

US-08-877-150B-36 (1-458) u49853p\_6

5. US-08-877-150B-36 (1-458)	100 110 120 130 140 150 160
u49853p_2 Initial Score = 11 Optimized Score = 159 Significance = -0.41 Residue Identity = 16% Matches = 62 Mismatches = 150 Gaps = 16	380 440 ARSAREAPLYSKVIPRAQRPG-AHAEDARGILPGRVPADQSPAGSGAYEDVAGGA-QTGGLGFNLRIGRP   S
110 LPHTLLDFWRLVWEFGVKV I SERVAAXVAIRTWXGAS- X	450 X KGPRDPPAEWTRV :   :   : AAVSASPGPLGRDXSWEGLSGSAATASHSQORTGHLFVRSQHCSGHRGVQVQALGGSGPPPPW 240 X 250
CREIENGRKRCERYWAQEQEPLQ-TGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVP   190	
210 220 230 240 250 250 270  SSPDHMLAMVEEARRLQGSGPEPLCV-HCSAGCGRTGVLCTVDXVRQLLLTQMIPPDFSLFDVVLKMRKQRP	
280 AAVQTEEOTRFLYHTVAQMECSTLQNASP-HYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLR : GLSASPXQRRQHXMQTSLSGPSRLHSRRNSALCTS-YSICPGQTTGFPAVLITFSPWWRRPAAS-K 170 210 220	
340 350 360 370 380 400 410  SISVPGSPGHAMADTYAEEGKRGAPAGAGSGTQTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLPG	
RVPADQSPAGSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV	
LWCRSVALRRAGGRGRPPARTPRFTARWLHVPSDRW 370 380 390	
6. US-08-877-150B-36-(1-458) 149853p_5	
Initial Score = 9 Optimized Score = 114 Significance = -0.42 Residue Identity = 13% Matches = 33 Mismatches = 188 Gaps = 13 Conservative Substitutions = 17	
170 180 190 200 210 x 220 230 KWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGGGRT	
240 250 260 200 200 300 GVLCTVDYVRQLLLFQMIPPDESLEDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMECSTLQNASPHYQNIKE : :       :	